



RECEIVED

JUL 09 2001

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Mahajan, Pramod B.
Zuo, Zhuang

<120> Poly ADP-Ribose Polymerase Gene and Its Uses

<130> 5718-34, 035718-174234

<140> 09/236,995

<141> 1999-01-26

<150> 60/072,785

<151> 1998-01-27

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 2949

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1)..(2949)

<220>

<221> misc_feature

<222> (1)..(2949)

<223> n=A, T, C, or G

<220>

<221> misc_feature

<222> (1)..(2949)

<223> Xaa=unknown

<400> 1

atg gcg gcg ccg cca aag gcg tgg aag gcg gag tat gcc aag tct ggg 48
Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
1 5 10 15

cgg gcc tcg tgc aag tca tgc cgg tcc cct atc gcc aag gac cag ctc 96
Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
20 25 30

cgt ctt ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg 144
Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
35 40 45

atg tgg aac cat gcc agg tgc atc ttc agc aag aag aac cag ata aaa 192
Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
50 55 60

tcc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg gat gat caa 240

Ser	Val	Asp	Asp	Val	Glu	Gly	Ile	Asp	Ala	Leu	Arg	Trp	Asp	Asp	Gln	
65					70					75					80	
gag aag ata cga aac tac gtt ggg agt gcc tca gct ggt aca agt tct 288																
Glu	Lys	Ile	Arg	Asn	Tyr	Val	Gly	Ser	Ala	Ser	Ala	Gly	Thr	Ser	Ser	
				85					90					95		
aca gct gct cct cct gag aaa tgt aca att gag att gct cca tct gcc 336																
Thr	Ala	Ala	Pro	Pro	Glu	Lys	Cys	Thr	Ile	Glu	Ile	Ala	Pro	Ser	Ala	
			100					105					110			
cgt act tca tgt aga cga tgc agt gaa aag att aca aaa gga tcg gtc 384																
Arg	Thr	Ser	Cys	Arg	Arg	Cys	Ser	Glu	Lys	Ile	Thr	Lys	Gly	Ser	Val	
		115					120					125				
cgt ctt tca gct aag ctt gag agt gaa ggt ccc aag ggt ata cca tgg 432																
Arg	Leu	Ser	Ala	Lys	Leu	Glu	Ser	Glu	Gly	Pro	Lys	Gly	Ile	Pro	Trp	
	130					135					140					
tat cat gcc aac tgt ttc ttt gag gta tcc ccg tct gca act gtt gag 480																
Tyr	His	Ala	Asn	Cys	Phe	Phe	Glu	Val	Ser	Pro	Ser	Ala	Thr	Val	Glu	
145				150					155					160		
aag ttc tca ggc tgg gat act ttg tcc gat gag gat aag aga acc atg 528																
Lys	Phe	Ser	Gly	Trp	Asp	Thr	Leu	Ser	Asp	Glu	Asp	Lys	Arg	Thr	Met	
				165				170					175			
ctc gat ctt gtt aaa aaa gat gtt ggc aac aat gaa caa aat aag ggt 576																
Leu	Asp	Leu	Val	Lys	Lys	Asp	Val	Gly	Asn	Asn	Glu	Gln	Asn	Lys	Gly	
		180						185				190				
tcc aag cgc aag aaa agt gaa aat gat att gat agc tac aaa tcc gcc 624																
Ser	Lys	Arg	Lys	Lys	Ser	Glu	Asn	Asp	Ile	Asp	Ser	Tyr	Lys	Ser	Ala	
	195					200						205				
agg tta gat gaa agt aca tct gaa ggt aca gtg cga aac aaa ggg caa 672																
Arg	Leu	Asp	Glu	Ser	Thr	Ser	Glu	Gly	Thr	Val	Arg	Asn	Lys	Gly	Gln	
	210					215				220						
ctt gta gac cca cgt ggt tcc aat act agt tca gct gat atc caa cta 720																
Leu	Val	Asp	Pro	Arg	Gly	Ser	Asn	Thr	Ser	Ser	Ala	Asp	Ile	Gln	Leu	
225					230					235				240		
aag ctt aag gag caa agt gac aca ctt tgg aag tta aag gat gga ctt 768																
Lys	Leu	Lys	Glu	Gln	Ser	Asp	Thr	Leu	Trp	Lys	Leu	Lys	Asp	Gly	Leu	
			245					250					255			
aag act cat gta tcg gct gct gaa tta agg gat atg ctt gag gct aat 816																
Lys	Thr	His	Val	Ser	Ala	Ala	Glu	Leu	Arg	Asp	Met	Leu	Glu	Ala	Asn	
		260					265					270				
ggg cag gat aca tca gga cca gaa agg cac cta ttg gat cgc tgt gcg 864																
Gly	Gln	Asp	Thr	Ser	Gly	Pro	Glu	Arg	His	Leu	Leu	Asp	Arg	Cys	Ala	
	275					280						285				
gat gga atg cta ttt gga gcg ctg ggt cct tgc cca gtc tgt gct aat 912																

Asp	Gly	Met	Leu	Phe	Gly	Ala	Leu	Gly	Pro	Cys	Pro	Val	Cys	Ala	Asn		
290						295					300						
ggc	atg	tac	tat	tat	aat	ggt	cag	tac	caa	tgc	agt	ggt	aat	gtg	tca	960	
Gly	Met	Tyr	Tyr	Tyr	Asn	Gly	Gln	Tyr	Gln	Cys	Ser	Gly	Asn	Val	Ser		
305					310					315					320		
gag	tgg	tcc	aag	tgt	aca	tac	tct	gcc	aca	gaa	cct	gtc	cgc	gtt	aag	1008	
Glu	Trp	Ser	Lys	Cys	Thr	Tyr	Ser	Ala	Thr	Glu	Pro	Val	Arg	Val	Lys		
				325					330						335		
aag	aag	tgg	caa	att	cca	cat	gga	aca	aag	aat	gat	tac	ctt	atg	aag	1056	
Lys	Lys	Trp	Gln	Ile	Pro	His	Gly	Thr	Lys	Asn	Asp	Tyr	Leu	Met	Lys		
			340					345					350				
tgg	ttc	aaa	tct	caa	aag	gtt	aag	aaa	cca	gag	agg	gtt	ctt	cca	cca	1104	
Trp	Phe	Lys	Ser	Gln	Lys	Val	Lys	Lys	Pro	Glu	Arg	Val	Leu	Pro	Pro		
		355					360					365					
atg	tca	cct	gag	aaa	tct	gga	agt	aaa	gca	act	cag	aga	aca	tca	ttg	1152	
Met	Ser	Pro	Glu	Lys	Ser	Gly	Ser	Lys	Ala	Thr	Gln	Arg	Thr	Ser	Leu		
	370					375					380						
ctg	tct	tct	aaa	ggg	ttg	gat	aaa	tta	agg	ttt	tct	gtt	gta	gga	caa	1200	
Leu	Ser	Ser	Lys	Gly	Leu	Asp	Lys	Leu	Arg	Phe	Ser	Val	Val	Gly	Gln		
385					390					395					400		
tca	aaa	gaa	gca	gca	aat	gag	tgg	att	gag	aag	ctc	aaa	ctt	gct	ggt	1248	
Ser	Lys	Glu	Ala	Ala	Asn	Glu	Trp	Ile	Glu	Lys	Leu	Lys	Leu	Ala	Gly		
			405						410					415			
gcc	aac	ttc	tat	gcc	agg	gtt	gtc	aaa	gat	att	gat	tgt	tta	att	gca	1296	
Ala	Asn	Phe	Tyr	Ala	Arg	Val	Val	Lys	Asp	Ile	Asp	Cys	Leu	Ile	Ala		
			420					425					430				
tgt	ggt	gag	ctc	gac	aat	gaa	aat	gct	gaa	gtc	agg	aaa	gca	agg	agg	1344	
Cys	Gly	Glu	Leu	Asp	Asn	Glu	Asn	Ala	Glu	Val	Arg	Lys	Ala	Arg	Arg		
		435				440						445					
ctg	aag	ata	cca	att	gta	agg	gag	ggt	tac	att	gga	gaa	tgt	gtt	aaa	1392	
Leu	Lys	Ile	Pro	Ile	Val	Arg	Glu	Gly	Tyr	Ile	Gly	Glu	Cys	Val	Lys		
	450					455					460						
aga	aca	aaa	tgc	tgc	cat	ttg	att	tgt	ata	aac	tgg	aat	gcc	tta	gag	1440	
Arg	Thr	Lys	Cys	Cys	His	Leu	Ile	Cys	Ile	Asn	Trp	Asn	Ala	Leu	Glu		
	465				470					475					480		
tcc	tca	aaa	ggc	mgt	act	gtc	act	gtt	aaa	gtt	aag	ggc	cga	agt	gct	1488	
Ser	Ser	Lys	Gly	Xaa	Thr	Val	Thr	Val	Lys	Val	Lys	Gly	Arg	Ser	Ala		
				485					490					495			
tgt	tca	tya	agt	cct	cyg	gtt	tgc	aag	aat	act	gct	cac	att	cct	tra	1536	
Cys	Ser	Xaa	Ser	Pro	Xaa	Val	Cys	Lys	Asn	Thr	Ala	His	Ile	Pro	Xaa		
		500						505					510				
gra	tgg	gaa	aag	cat	ata	caa	tgc	amc	ctt	aaa	cat	gtt	ctg	acc	tgn	1584	

Xaa	Trp	Glu	Lys	His	Ile	Gln	Cys	Xaa	Leu	Lys	His	Val	Leu	Thr	Xaa	
515							520					525				
cac	nag	gtg	tgy	aca	ggc	tac	tat	gta	ctc	cag	atc	att	gaa	cag	gat	1632
His	Xaa	Val	Cys	Thr	Gly	Tyr	Tyr	Val	Leu	Gln	Ile	Ile	Glu	Gln	Asp	
530						535					540					
gat	ggg	tct	gag	tgc	tac	gta	ttt	cgt	aag	tgg	gga	cgg	gtt	ggg	agt	1680
Asp	Gly	Ser	Glu	Cys	Tyr	Val	Phe	Arg	Lys	Trp	Gly	Arg	Val	Gly	Ser	
545					550					555					560	
gag	aaa	att	gga	ggg	caa	aaa	ctg	gag	gag	atg	tca	aaa	act	gag	gca	1728
Glu	Lys	Ile	Gly	Gly	Gln	Lys	Leu	Glu	Glu	Met	Ser	Lys	Thr	Glu	Ala	
				565					570					575		
atc	aag	gaa	ttc	aaa	aga	tta	ttt	ctt	gag	aag	act	gga	aac	tca	tgg	1776
Ile	Lys	Glu	Phe	Lys	Arg	Leu	Phe	Leu	Glu	Lys	Thr	Gly	Asn	Ser	Trp	
			580					585					590			
gaa	gct	tgg	gaa	tgt	aaa	acc	aat	ttt	cgg	aag	cag	cct	ggg	aga	ttt	1824
Glu	Ala	Trp	Glu	Cys	Lys	Thr	Asn	Phe	Arg	Lys	Gln	Pro	Gly	Arg	Phe	
		595					600					605				
tac	cca	ctt	gat	gtt	gat	tat	ggg	gtt	aag	aaa	gca	cca	aaa	cgg	aaa	1872
Tyr	Pro	Leu	Asp	Val	Asp	Tyr	Gly	Val	Lys	Lys	Ala	Pro	Lys	Arg	Lys	
610						615					620					
gat	atc	agt	gaa	atg	aaa	agt	tct	ctt	gct	cct	caa	ttg	cta	gaa	ctc	1920
Asp	Ile	Ser	Glu	Met	Lys	Ser	Ser	Leu	Ala	Pro	Gln	Leu	Leu	Glu	Leu	
625					630					635					640	
atg	aag	atg	ctt	ttc	aat	gtg	gag	aca	tat	aga	gct	gct	atg	atg	gaa	1968
Met	Lys	Met	Leu	Phe	Asn	Val	Glu	Thr	Tyr	Arg	Ala	Ala	Met	Met	Glu	
				645					650					655		
ttt	gaa	awt	aat	atg	tca	gaa	atg	cct	ctt	ggg	aag	cta	agc	mag	gra	2016
Phe	Glu	Xaa	Asn	Met	Ser	Glu	Met	Pro	Leu	Gly	Lys	Leu	Ser	Xaa	Xaa	
			660					665					670			
aat	att	gag	raa	gga	ttt	gaa	gca	tta	act	krp	rta	cmg	rat	tta	ttt	2064
Asn	Ile	Glu	Xaa	Gly	Phe	Glu	Ala	Leu	Thr	Xaa	Xaa	Xaa	Xaa	Leu	Phe	
		675					680					685				
gaa	gga	cac	cgc	tna	tca	agc	act	ggc	ttg	ttr	gag	aaa	gct	naa	ttg	2112
Glu	Gly	His	Arg	Xaa	Ser	Ser	Thr	Gly	Leu	Xaa	Glu	Lys	Ala	Xaa	Leu	
		690				695					700					
ttg	ytg	sga	gcm	ats	syt	ttt	tca	ctc	tta	tcc	ctt	cta	ttc	atc	ctc	2160
Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Ser	Leu	Leu	Ser	Leu	Leu	Phe	Ile	Leu	
705					710					715					720	
ata	tta	tac	ggg	atg	agg	atg	att	tca	tat	tca	aag	gcg	aaa	atg	ctt	2208
Ile	Leu	Tyr	Gly	Met	Arg	Met	Ile	Ser	Tyr	Ser	Lys	Ala	Lys	Met	Leu	
				725					730					735		
gaa	gct	ctg	cag	gat	att	gaa	att	gct	tca	aag	ata	gtt	ggc	ttc	gat	2256

Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp	
740 745 750	
agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa ctt cac tgt	2304
Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys	
755 760 765	
gac atc acc ccg ctg gct cac gat agt gaa gat tac aag tta att gag	2352
Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu	
770 775 780	
cag tat ctc ctc aac aca cat gct cct act cac aag gac tgg tcg ctg	2400
Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu	
785 790 795 800	
gaa ctg gag gaa gtt ttt tca ctt gat cga gat gga gaa ctt aat aag	2448
Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys	
805 810 815	
tac tca aga tat aaa aat aat ctg cat aac aag atg cta tta tgg cac	2496
Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His	
820 825 830	
ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa ggg cta aga	2544
Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg	
835 840 845	
att gca cct cct gag gca cct gtt act ggc tat atg ttc ggc aaa ggc	2592
Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly	
850 855 860	
ctc tac ttt gca gat cta gta agc aag agc gca caa tac tgt tat gtg	2640
Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val	
865 870 875 880	
gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta	2688
Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu	
885 890 895	
gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct cca	2736
Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro	
900 905 910	
aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag	2784
Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu	
915 920 925	
tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc aag	2832
Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys	
930 935 940	
ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac	2880
Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr	
945 950 955 960	
atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg	2928

Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val
 965 970 975

cgt ttc cat cac aag agg tag
 Arg Phe His His Lys Arg
 980

2949

<210> 2
 <211> 982
 <212> PRT
 <213> Zea mays
 <220>
 <221> misc_feature
 <222> (1)..(982)
 <223> Xaa=unknown

<400> 2
 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
 1 5 10 15
 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
 20 25 30
 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
 35 40 45
 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
 50 55 60
 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
 65 70 75 80
 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
 85 90 95
 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
 100 105 110
 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
 115 120 125
 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
 130 135 140
 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
 145 150 155 160
 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
 165 170 175
 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
 180 185 190
 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
 195 200 205
 Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
 210 215 220
 Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
 225 230 235 240
 Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
 245 250 255
 Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
 260 265 270
 Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
 275 280 285

Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
 290 295 300
 Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
 305 310 315 320
 Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
 325 330 335
 Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
 340 345 350
 Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
 355 360 365
 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
 370 375 380
 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
 385 390 395 400
 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
 405 410 415
 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
 420 425 430
 Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
 435 440 445
 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
 450 455 460
 Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
 465 470 475 480
 Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala
 485 490 495
 Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
 500 505 510
 Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
 515 520 525
 His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp
 530 535 540
 Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
 545 550 555 560
 Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
 565 570 575
 Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
 580 585 590
 Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
 595 600 605
 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
 610 615 620
 Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu
 625 630 635 640
 Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
 645 650 655
 Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa
 660 665 670
 Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
 675 680 685
 Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
 690 695 700
 Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
 705 710 715 720
 Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
 725 730 735

Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
 740 745 750
 Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
 755 760 765
 Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
 770 775 780
 Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu
 785 790 795 800
 Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys
 805 810 815
 Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His
 820 825 830
 Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg
 835 840 845
 Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly
 850 855 860
 Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val
 865 870 875 880
 Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu
 885 890 895
 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
 900 905 910
 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
 915 920 925
 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys
 930 935 940
 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr
 945 950 955 960
 Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val
 965 970 975
 Arg Phe His His Lys Arg
 980

<210> 3
 <211> 474
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(474)

<400> 3
 aac aag atg cta tta tgg cac ggt tca agg ttg acg aat ttt gtg gga 48
 Asn Lys Met Leu Leu Trp His Gly Ser Arg Leu Thr Asn Phe Val Gly
 1 5 10 15
 att ctt agt caa ggg cta aga att gca cct cct gag gca cct gtt act 96
 Ile Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr
 20 25 30
 ggc tat atg ttc ggc aaa ggc ctc tac ttt gca gat cta gta agc aag 144
 Gly Tyr Met Phe Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys
 35 40 45

agc gca caa tac tgt tat gtg gat agg aat aat cct gta ggt ttg atg 192
 Ser Ala Gln Tyr Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met
 50 55 60

ctt ctt tct gag gtt gct tta gga gac atg tat gaa cta aag aaa gcc 240
 Leu Leu Ser Glu Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala
 65 70 75 80

acg tcc atg gac aaa cct cca aga ggg aag cat tcg acc aag gga tta 288
 Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu
 85 90 95

ggc aaa acc gtg cca ctg gag tca gag ttt gtg aag tgg agg gat gat 336
 Gly Lys Thr Val Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp
 100 105 110

gtc gta gtt ccc tgc ggc aag ccg gtg cca tca tca att agg agc tct 384
 Val Val Val Pro Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser
 115 120 125

gaa ctc atg tac aat gag tac atc gtc tac aac aca tcc cag gtg aag 432
 Glu Leu Met Tyr Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys
 130 135 140

atg cag ttc ttg ctg aag gtg cgt ttc cat cac aag agg tag 474
 Met Gln Phe Leu Leu Lys Val Arg Phe His His Lys Arg
 145 150 155

<210> 4

<211> 157

<212> PRT

<213> Zea mays

<400> 4

Asn Lys Met Leu Leu Trp His Gly Ser Arg Leu Thr Asn Phe Val Gly
 1 5 10 15
 Ile Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr
 20 25 30
 Gly Tyr Met Phe Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys
 35 40 45
 Ser Ala Gln Tyr Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met
 50 55 60
 Leu Leu Ser Glu Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala
 65 70 75 80
 Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu
 85 90 95
 Gly Lys Thr Val Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp
 100 105 110
 Val Val Val Pro Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser
 115 120 125
 Glu Leu Met Tyr Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys
 130 135 140
 Met Gln Phe Leu Leu Lys Val Arg Phe His His Lys Arg
 145 150 155

<210> 5
<211> 530
<212> DNA
<213> Zea mays

<400> 5

ctcgtgcaag tcatgccggt cccctatcgc caaggaccag ctccgtcttg gcaagatggg 60
tcaggcgtca cagttcgacg gcttcatgcc gatgtggaac catgccagggt gcatcttcag 120
caagaagaac cagataaaat ccgttgacga tggtgaaggg atagatgcac ttagatggga 180
tgatcaagag aagatacgaa actacgttgg gagtgcctca gctggtacaa gttctacagc 240
tgctcctcct gagaaatgta caattgagat tgctccatct gcccgactt catgtagacg 300
atgcagtga aagattacaa aaggatcggg ccgtctttca gctaagcttg agagtgaagg 360
tccaagggt ataccatggg atcatgcaa ctgtttcttt gaggtatccc cgtctgcaac 420
tggtgagaag ttctcaggct gggatacttt gtccgatgag gataagagaa ccatgctcga 480
tcttgtaaaa aaagatgttg gcaacaatga acaaaataag gggtccaagc 530
